Supplementary Fig. 1. Example of the hidden Markov model emission probabilities calculated for sample nf0h3ab, as generated by q master 'segment'. Each trace shows the frequency of different bin input states (indicated on the X axis) for each of ten different output states (indicated in the legend). Probabilities were trained based on observed bin RPKM in annotated genes and subsequently applied genome wide.

nf0h3ab Hidden Markov Model, bin=1000

